

SEQUENCE LISTING

(1) GENERAL INFORMATION:

APPLICANT:

5 NAME: The Procter & Gamble Company
STREET: One Procter & Gamble Plaza
CITY: Cincinnati, OHIO
COUNTRY: USA
POSTAL CODE: 45202

10 TITLE OF INVENTION: Detergent compositions comprising a mannanase and a
soil release polymer.

NUMBER OF SEQUENCES: 6

COMPUTER READABLE FORM:

15 MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release # 1.0 Version 1.25 (EPO)

SEQ ID NO:1

SEQUENCE CHARACTERISTICS:

25 LENGTH: 1407 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

30 MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE

FEATURE:

NAME/KEY: CDS
35 LOCATION: 1-1482

PCT/US98/12027

SEQUENCE DESCRIPTION: SEQ ID NO: 1

5 ATGAAAAAAAGTTACACAGATTATCATTAAATTTCACACTTATAATA
TTTATGTTGATGGCAATAACGTTATATGACGAAATGGCAGCCATTGTCAT
GAGAGGTATTAACCATGGACATGCTGGTATAAAGACACCGCTCAACAGCT
ATTCTGCCATTGCAGAGCAAGGCGCCAACACGATTGCTATTGTTTATCAG
10 ATGGCGGTCAATGGAAAAAGACGACATTGACACCATTGTAAGTCATTG
AGCTTGCAGCAAATAATGGTGGCTGCTGAAGTTCATGATGCCA
CGGGTCGCGATTGCGCAGTGATTAAATCGAGCCGTTGATTGGATAG
AAATGAAAGATGCGCTTATCGTAAAGAAGATACGGTTATTAAACATTGCA
AACGAGTGGTATGGAGTTGGATGGCTCAGCTGGCCGATGGCTATATT
15 GATGTCATTCCGAAGCTTCGCGATGCCGGCTAACACACACCTTAATGGTTG
ATGCAGCAGGATGGGGCAATATCGCAATCTATTGATTACGGACAAG
ATGTGTTAATGCAAGATCCGTTAAAAAACAGATGTTCTCCATCCATATGTAT
GAGTATGCTGGTGGTATGCTAACACTGTTAGTCAAATATTGATAGAGTC
TAGATCAAGACCTTGCTCGTAATAGGTGAATTGGTCAAGACATACTGA
20 TGGTGATGTTGATGAAGATACAATCCTAGTTATTCTGAAGAAACTGGCACA
GGGTGGCTCGCTGGCTGGAAAGGCAACAGTACCGAATGGACTATTAA
GACCTTCAGAAGACTGGCTGGCAACATTAACTGATTGGGGAAATAGAA
TTGTCACGGGCCATGGCTACAGGAAACCTCAAACCTCCACCGTAT
TTACAGATGATAACGGTGGTCACCCCTGAACCGCCAAGTGTACTACCTGTA
TGACTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG
25 GCCCTTGGTCCGTAACAGAATGGGTGCTCAGGTAACTACTCTTAAAAGC
CGATGTAATTAAACCTCAAATTCTCACATGAACTGTATAGTGAACAAAGTC
GTAATCTACACGGATACTCTCAGCTAACGCAACCGTTGCCATGCCATTG
GGAAATCCCGTAATGGCATGAATGCAAGACTTACGTGAAAACGGGCTC
TGATTATACGGCATAGCGGTCTTACACGTATCAATAGCTCAAACGTA
30 GGAACAAACGTTATCTTGTATTAAACACATGAAAATAGTCATGTTAG
GGAAATAGGCGTGCAATTTCAGCGGAGATAATAGCAGTGGTCAAACGTC
TCTATACGTTGATAACGTTACTTAAAGATAG

PCT/US98/12027

SEQ ID NO:25 **SEQUENCE CHARACTERISTICS:**

LENGTH: 493 amino acids

TYPE: amino acid

TOPOLOGY: linear

10 **MOLECULE TYPE:** protein**SEQUENCE DESCRIPTION:** SEQ ID NO: 2

MKKKLSQIYHLIICTLIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN
HGHAWYKDTASTAIPAIAEQGANTIRIVLSDGGQWEKDDIDTIREVIELAEQNKM

15 VAVVEVHDATGRDSRSIDLNRADVYWIEMKDALIGKEDTVIINIANEWYGSWDGS
AWADGYIDVIPKLRDAGLTHLMVDAAGWGQYPQSIHDYQGDVFNADPLKNTM
FSIHYMYEYAGGDANTVRSNIDRVIDQDLALVIGEFGHRHTDGDVDEDTILSYSEE
TGTGWLAWSWKGNSTEWLDYLDLSEDWAGQHLTDWGNRIVHGADGLQETSKP
20 STVFTDDNGGHPEPPTATTLYDFEGSTQGWHGSNVTGGPWSVTEWGASGNY
SLKADVNLTSNSSHELYSEQSRNLHGSQLNATVRHANWGNPGNGMNARLYV
KTGSDYTWHSGPFTRINSSNSGTTLSFDLNNIENSHHVREIGVQFSAADNSSGQ
TALYVDNVTLR

25 **SEQ ID NO:3****SEQUENCE CHARACTERISTICS:**

LENGTH: 1407 base pairs

TYPE: nucleic acid

30 **STRANDEDNESS:** single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA35 **SEQUENCE DESCRIPTION:** SEQ ID NO: 3

ATGAAAAAAAAGTTATCACAGATTATCATTAAATTATTCACACTTATAATA
AGTGTGGAAATAATGGGGATTACAACGTCCCCATCAGCAGCAAGTACAGGC
TTTATGTTGATGGCAATACGTTATATGACGCAAATGGGCAGCCATTGTCAT
GAGAGGTATTAACCATGGACATGCTTGGTATAAAGACACCGCTTCAACAGCT
5 ATTCCCTGCCATTGCAGAGCAAGGCAGCAACACGATTGCTATTGTTTATCAG
ATGGCGGTCAATGGGAAAAGACGACATTGACACCATTGCTGAAGTCATTG
AGCTTGCAGGAGCAAAATAAAATGGTGGCTGTCGTGAAGTTCATGATGCCA
CGGGTCGCGATTGCGCAGTGATTAAATCGAGCCGTTGATTATTGGATAG
AAATGAAAGATGCGCTTATCGTAAAGAAGATACTGGTTATTATTAAACATTGCA
10 AACGAGTGGTATGGGAGTTGGGATGGCTCAGCTTGGGCCATGGCTATAATT
GATGTCATTCCGAAGCTTCGCGATGCCGGCTAACACACACCTTAATGGTTG
ATGCAGCAGGATGGGGCAATATCCGCAATCTATTGATTACGGACAAG
ATGTGTTAACGATCCGTTAAAAAATACGATGTTCTCCATCCATATGTAT
GAGTATGCTGGTGGTGTGCTAACACTGTTAGATCAAATATTGATAGAGTC
15 TAGATCAAGACCTTGCCTCGTAATAGGTGAATTGGCTCATAGACATACTGA
TGGTGTGTTGATGAAGATACAATCCTAGTTATTCTGAAGAAACTGGCACA
GGGTGGCTCGCTTGGTCTTGGAAAGGCAACAGTACCGAATGGGACTATT
GACCTTCAGAAGACTGGGCTGGTCAACATTAACTGATTGGGGAATAGAA
TTGTCCACGGGGCCGATGGCTTACAGGAAACCTCCAAACCATCCACCGTAT
20 TTACAGATGATAACGGTGGTCACCCCTGAACCGCCAAGTGTACTACCTTGTA
TGACTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG
GCCCTTGGTCCGTAACAGAATGGGGTGTTCAGGTAACTACTCTTAAAGC
CGATGTAATTAAACCTCAAATTCTCACATGAAGTGTATAGTGAACAAAGTC
GTAATCTACACGGATACTCTCAGCTCAACGCAACCGTTGCCATGCCAATTG
25 GGGAAATCCCGTAATGGCATGAATGCAAGACTTACGTGAAAACGGGCTC
TGATTATACATGGCATAGCGGTCTTTACACGTATCAATAGCTCCAACCTCA
GGAACAAACGTTATCTTGTATTAAACAACATCGAAAATATCATCATGTTAGG
GAAATAG

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SEQ ID NO:4**SEQUENCE CHARACTERISTICS:**

LENGTH: 468 amino acids

35 TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4

5 MKKKLSQIYHLIICLIIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN
HGHAWYKDTASTAIPAIAEQGANTIRIVLSDGGQWEKDDIDTIREVIELAEQNKM
VAVVEVHDATGRDSRSIDLNAVDYWIEMKDALIGKEDTVIINIANEWYGSWDGS
AWADGYIDVIPKLRDAGLTHLMVDAAGWGQYPQSIHDYQGDVFNAADPLKNTM
FSIHMYEYAGGDANTVRSNIDRVIDQDLALVIGEFGHRHTDGDVDEDTILSYSEE
10 TGTGWLAWSWKGNSTEWDYLDLSEDWAGQHLDWGNRIVHGADGLQETSKP
STVFTDDNGGHPEPPTATTLYDFEGSTQGWHGSNVTGGPWSVTEWGASGNY
SLKADVNLTSNSSHELYSEQSRNLHGYSQLNATVRHANWGNPGNGMNARLYV
KTGSDYTWHSGPFTRINSSNSGTTLSFDLNNIENIIMLGK

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SEQ ID NO:5

SEQUENCE CHARACTERISTICS:

LENGTH: 1029 base pairs

20 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

25

SEQUENCE DESCRIPTION SEQ ID No:5

5' AAT TGG CGC ATA CTG TGT CGC CTG TGA ATC CTA ATG CCC AGC
AGA CAA CAA AAA CAG TGA TGA ACT GGC TTG CGC ACC TGC CGA ACC
30 GAA CGG AAA ACA GAG TCC TTT CCG GAG CGT TCG GAG GTT ACA GCC
ATG ACA CAT TTT CTA TGG CTG AGG CTG ATA GAA TCC GAA GCG CCA
CCG GGC AAT CGC CTG CTA TTT ATG GCT GCG ATT ATG CCA GAG GAT
GGC TTG AAA CAG CAA ATA TTG AAG ATT CAA TAG ATG TAA GCT GCA
ACG GCG ATT TAA TGT CGT ATT GGA AAA ATG GCG GAA TTC CGC AAA
35 TCA GTT TGC ACC TGG CGA ACC CTG CTT TTC AGT CAG GGC ATT TTA
AAA CAC CGA TTA CAA ATG ATC AGT ATA AAA ACA TAT TAG ATT CAG

CAA CAG CGG AAG GGA AGC GGC TAA ATG CCA TGC TCA GCA AAA TTG
CTG ACG GAC TTC AAG AGT TGG AGA ACC AAG GTG TGC CTG TTC TGT
TCA GGC CGC TGC ATG AAA TGA ACG GCG AAT GGT TTT GGT GGG GAC
TCA CAT CAT ATA ACC AAA AGG ATA ATG AAA GAA TCT CTC TAT ATA
5 AAC AGC TCT ACA AGA AAA TCT ATC ATT ATA TGA CCG ACA CAA GAG
GAC TTG ATC ATT TGA TTT GGG TTT ACT CTC CCG ACG CCA ACC GAG
ATT TTA AAA CTG ATT TTT ACC CCG GCG CGT CTT ACG TGG ATA TTG
TCG GAT TAG ATG CGT ATT TTC AAG ATG CCT ACT CGA TCA ATG GAT
ACG ATC AGC TAA CAG CGC TTA ATA AAC CAT TTG CTT TTA CAG AAG
10 TCG GCC CGC AAA CAG CAA ACG GCA GCT TCG ATT ACA GCC TGT TCA
TCA ATG CAA TAA AAC AAA AAT ATC CTA AAA CCA TTT ACT TTC TGG
CAT GGA ATG ATG AAT GGA GCG CAG CAG TAA ACA AGG GTG CTT CAG
CTT TAT ATC ATG ACA GCT GGA CAC TCA ACA AGG GAG AAA TAT GGA
ATG GTG ATT CTT TAA CGC CAA TCG TTG AGT GAA TCC GGG ATC 3'
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SEQ ID NO:6**SEQUENCE CHARACTERISTICS:**20 **LENGTH:** 363 amino acids**TYPE:** amino acid**TOPOLOGY:** linear**MOLECULE TYPE:** protein25 **SEQUENCE DESCRIPTION:** SEQ ID NO: 6

ydhT

1

LFKKHTISLLIIFLLASAVLAKPIEAHTVSPVNPNAQQTTKTVMNWL AHL 50

30 ydhT

51

PNRTENRVLSGAFGGYSHDTFSMAEADRIRSATGQSPAIYGCDYARGWLE 100

ydhT

101

TANIEDSIDVSCNGDLMSYWKGIGIPQISLHLANPAFQSGHFKTPITNDQ 150

ydhT

151

35 YKNILDSATAEGKRLNAMLSKIADGLQELENQGVPVLFRPLHEMNGEWFW 200

0094335501-040500

5 ydhT 201
WGLTSYNQKDNERISLYKQLYKKIYHYMTDTRGLDHЛИWVYSPDANRDFK 250
ydhT 251
TDFYPGASYVDIVGLDAYFQDAYSINGYDQLTALNKPFAFTEVGPQTANG 300
5 ydhT 301
SFDYSLFINAIKQKYPKTIYFLAWNDEWSAAVNKGASALYHDSWTLNKGЕ 350
ydhT 351
IWNGDSLTPIVE*. 363

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